

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/550,924  
Source: 1 Fwd  
Date Processed by STIC: 11/6/06

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/550,924

DATE: 11/06/2006

TIME: 10:03:26

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3 <110> APPLICANT: Furusawa, Mitsuru  
 6 <120> TITLE OF INVENTION: METHOD AND SYSTEM FOR RAPIDLY CONFERRING  
 7 A DESIRED TRAIT TO AN ORGANISM  
 9 <130> FILE REFERENCE: 690116.401USPC  
 11 <140> CURRENT APPLICATION NUMBER: US 10/550,924  
 C--> 12 <141> **CURRENT FILING DATE: 2005-09-28**  
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/004378  
 15 <151> PRIOR FILING DATE: 2004-03-26  
 17 <150> PRIOR APPLICATION NUMBER: JP 2003-092898  
 18 <151> PRIOR FILING DATE: 2003-03-28  
 20 <150> PRIOR APPLICATION NUMBER: US 10/684,141  
 21 <151> PRIOR FILING DATE: 2003-10-10  
 23 <160> NUMBER OF SEQ ID NOS: 95  
 25 <170> SOFTWARE: PatentIn Ver. 2.1  
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 28 <211> LENGTH: 3551  
 29 <212> TYPE: DNA  
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 37 aatcaaacgg caatcaatag atcatggtgt tgggaagtga cctggttcaa caatagagat 300  
 38 tattccgagt gattcttttc gaaaatataa tagtcaaggc ttcaaagcaa aggatacaga 360  
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95 &lt;210&gt; SEQ ID NO: 2

96 &lt;211&gt; LENGTH: 1097

97 &lt;212&gt; TYPE: PRT

98 <213> ORGANISM: *Saccharomyces cerevisiae*

100 &lt;400&gt; SEQUENCE: 2

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105             20             25             30
107 His Gly Val Gly Ser Glu Pro Val Ser Thr Ile Glu Ile Ile Pro Ser
108             35             40             45
110 Asp Ser Phe Arg Lys Tyr Asn Ser Gln Gly Phe Lys Ala Lys Asp Thr
111   50             55             60

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117 85 90 95
119 Phe Glu Arg Lys Lys Leu Pro Thr Asp Phe Asp Pro Ser Leu Tyr Asp
120 100 105 110
122 Ile Ser Phe Gln Gln Ile Asp Ala Glu Gln Ser Val Leu Asn Gly Ile
123 115 120 125
125 Lys Asp Glu Asn Thr Ser Thr Val Val Arg Phe Phe Gly Val Thr Ser
126 130 135 140
128 Glu Gly His Ser Val Leu Cys Asn Val Thr Gly Phe Lys Asn Tyr Leu
129 145 150 155 160
131 Tyr Val Pro Ala Pro Asn Ser Ser Asp Ala Asn Asp Gln Glu Gln Ile
132 165 170 175
134 Asn Lys Phe Val His Tyr Leu Asn Glu Thr Phe Asp His Ala Ile Asp
135 180 185 190
137 Ser Ile Glu Val Val Ser Lys Gln Ser Ile Trp Gly Tyr Ser Gly Asp
138 195 200 205
140 Thr Lys Leu Pro Phe Trp Lys Ile Tyr Val Thr Tyr Pro His Met Val
141 210 215 220
143 Asn Lys Leu Arg Thr Ala Phe Glu Arg Gly His Leu Ser Phe Asn Ser
144 225 230 235 240
146 Trp Phe Ser Asn Gly Thr Thr Thr Tyr Asp Asn Ile Ala Tyr Thr Leu
147 245 250 255
149 Arg Leu Met Val Asp Cys Gly Ile Val Gly Met Ser Trp Ile Thr Leu
150 260 265 270
152 Pro Lys Gly Lys Tyr Ser Met Ile Glu Pro Asn Asn Arg Val Ser Ser
153 275 280 285
155 Cys Gln Leu Glu Val Ser Ile Asn Tyr Arg Asn Leu Ile Ala His Pro
156 290 295 300
158 Ala Glu Gly Asp Trp Ser His Thr Ala Pro Leu Arg Ile Met Ser Phe
159 305 310 315 320
161 Asp Ile Glu Cys Ala Gly Arg Ile Gly Val Phe Pro Glu Pro Glu Tyr
162 325 330 335
164 Asp Pro Val Ile Gln Ile Ala Asn Val Val Ser Ile Ala Gly Ala Lys
165 340 345 350
167 Lys Pro Phe Ile Arg Asn Val Phe Thr Leu Asn Thr Cys Ser Pro Ile
168 355 360 365
170 Thr Gly Ser Met Ile Phe Ser His Ala Thr Glu Glu Glu Met Leu Ser
171 370 375 380
173 Asn Trp Arg Asn Phe Ile Ile Lys Val Asp Pro Asp Val Ile Ile Gly
174 385 390 395 400
176 Tyr Asn Thr Thr Asn Phe Asp Ile Pro Tyr Leu Leu Asn Arg Ala Lys
177 405 410 415
179 Ala Leu Lys Val Asn Asp Phe Pro Tyr Phe Gly Arg Leu Lys Thr Val
180 420 425 430
182 Lys Gln Glu Ile Lys Glu Ser Val Phe Ser Ser Lys Ala Tyr Gly Thr
183 435 440 445
185 Arg Glu Thr Lys Asn Val Asn Ile Asp Gly Arg Leu Gln Leu Asp Leu

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189 465      470      475      480
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192      485      490      495
194 Ser Ile Ile Ser Asp Leu Gln Asn Gly Asp Ser Glu Thr Arg Arg Arg
195      500      505      510
197 Leu Ala Val Tyr Cys Leu Lys Asp Ala Tyr Leu Pro Leu Arg Leu Met
198      515      520      525
200 Glu Lys Leu Met Ala Leu Val Asn Tyr Thr Glu Met Ala Arg Val Thr
201      530      535      540
203 Gly Val Pro Phe Ser Tyr Leu Leu Ala Arg Gly Gln Gln Ile Lys Val
204 545      550      555      560
206 Val Ser Gln Leu Phe Arg Lys Cys Leu Glu Ile Asp Thr Val Ile Pro
207      565      570      575
209 Asn Met Gln Ser Gln Ala Ser Asp Asp Gln Tyr Glu Gly Ala Thr Val
210      580      585      590
212 Ile Glu Pro Ile Arg Gly Tyr Tyr Asp Val Pro Ile Ala Thr Leu Asp
213      595      600      605
215 Phe Asn Ser Leu Tyr Pro Ser Ile Met Met Ala His Asn Leu Cys Tyr
216      610      615      620
218 Thr Thr Leu Cys Asn Lys Ala Thr Val Glu Arg Leu Asn Leu Lys Ile
219 625      630      635      640
221 Asp Glu Asp Tyr Val Ile Thr Pro Asn Gly Asp Tyr Phe Val Thr Thr
222      645      650      655
224 Lys Arg Arg Arg Gly Ile Leu Pro Ile Ile Leu Asp Glu Leu Ile Ser
225      660      665      670
227 Ala Arg Lys Arg Ala Lys Lys Asp Leu Arg Asp Glu Lys Asp Pro Phe
228      675      680      685
230 Lys Arg Asp Val Leu Asn Gly Arg Gln Leu Ala Leu Lys Ile Ser Ala
231      690      695      700
233 Asn Ser Val Tyr Gly Phe Thr Gly Ala Thr Val Gly Lys Leu Pro Cys
234 705      710      715      720
236 Leu Ala Ile Ser Ser Ser Val Thr Ala Tyr Gly Arg Thr Met Ile Leu
237      725      730      735
239 Lys Thr Lys Thr Ala Val Gln Glu Lys Tyr Cys Ile Lys Asn Gly Tyr
240      740      745      750
242 Lys His Asp Ala Val Val Val Tyr Gly Asp Thr Asp Ser Val Met Val
243      755      760      765
245 Lys Phe Gly Thr Thr Asp Leu Lys Glu Ala Met Asp Leu Gly Thr Glu
246      770      775      780
248 Ala Ala Lys Tyr Val Ser Thr Leu Phe Lys His Pro Ile Asn Leu Glu
249 785      790      795      800
251 Phe Glu Lys Ala Tyr Phe Pro Tyr Leu Leu Ile Asn Lys Lys Arg Tyr
252      805      810      815
254 Ala Gly Leu Phe Trp Thr Asn Pro Asp Lys Phe Asp Lys Leu Asp Gln
255      820      825      830
257 Lys Gly Leu Ala Ser Val Arg Arg Asp Ser Cys Ser Leu Val Ser Ile
258      835      840      845

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264 865      870      875      880
266 Arg Val Asp Ile Ser Lys Leu Ile Ile Ser Lys Thr Leu Ala Pro Asn
267      885      890      895
269 Tyr Thr Asn Pro Gln Pro His Ala Val Leu Ala Glu Arg Met Lys Arg
270      900      905      910
272 Arg Glu Gly Val Gly Pro Asn Val Gly Asp Arg Val Asp Tyr Val Ile
273      915      920      925
275 Ile Gly Gly Asn Asp Lys Leu Tyr Asn Arg Ala Glu Asp Pro Leu Phe
276      930      935      940
278 Val Leu Glu Asn Asn Ile Gln Val Asp Ser Arg Tyr Tyr Leu Thr Asn
279 945      950      955      960
281 Gln Leu Gln Asn Pro Ile Ile Ser Ile Val Ala Pro Ile Ile Gly Asp
282      965      970      975
284 Lys Gln Ala Asn Gly Met Phe Val Val Lys Ser Ile Lys Ile Asn Thr
285      980      985      990
287 Gly Ser Gln Lys Gly Gly Leu Met Ser Phe Ile Lys Lys Val Glu Ala
288      995      1000      1005
290 Cys Lys Ser Cys Lys Gly Pro Leu Arg Lys Gly Glu Gly Pro Leu Cys
291      1010      1015      1020
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294 1025      1030      1035      1040
296 Asp Val Arg Asp Leu Glu Glu Lys Tyr Ser Arg Leu Trp Thr Gln Cys
297      1045      1050      1055
299 Gln Arg Cys Ala Gly Asn Leu His Ser Glu Val Leu Cys Ser Asn Lys
300      1060      1065      1070
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311 <212> TYPE: DNA
312 <213> ORGANISM: Saccharomyces cerevisiae
314 <400> SEQUENCE: 3 .
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L:1218 M:112 C: (48) String data converted to lower case,  
L:1230 M:112 C: (48) String data converted to lower case,  
L:1242 M:112 C: (48) String data converted to lower case,  
L:7903 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 90  
L:7931 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 90  
L:8302 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 92  
L:8330 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 92